



SEQUENCE LISTING

(1) GENERAL INFORMATION:

COPIES
ORIGINALS

(i) APPLICANT: Choi, Yongwon
Wong, Brian
Josien, Regis
Steinman, Ralph

(ii) TITLE OF INVENTION: A PROTEIN BELONGING TO THE TNF SUPERFAMILY INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING SAME, AND METHODS OF USE THEREOF

(iii) NUMBER OF SEQUENCES: 18

(iv) CORRESPONDENCE ADDRESS:

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(E) COUNTRY: USA
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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) ATTORNEY/AGENT INFORMATION:

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(B) REGISTRATION NUMBER: 26,742
(C) REFERENCE/DOCKET NUMBER: 600-1-200 CIP N

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1823 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAG ATG GAT CCT AAT AGA ATA TCA GAA GAT GGC ACT CAC TGC ATT TAT
48

Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Gly Thr His Cys Ile Tyr
1 5 10 15

AGA ATT TTG AGA CTC CAT GAA AAT GCA GAT TTT CAA GAC ACA ACT CTG
96

Arg Ile Leu Arg Leu His Glu Asn Ala Asp Phe Gln Asp Thr Thr Leu
20 25 30

GAG AGT CAA GAT ACA AAA TTA ATA CCT GAT TCA TGT AGG AGA ATT AAA
144

Glu Ser Gln Asp Thr Lys Leu Ile Pro Asp Ser Cys Arg Arg Ile Lys
35 40 45

CAG GCC TTT CAA GGA GCT GTG CAA AAG GAA TTA CAA CAT ATC GTT GGA
192

Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly
50 55 60

TCA CAG CAC ATC AGA GCA GAG AAA GCG ATG GTG GAT GGC TCA TGG TTA
240

Ser Gln His Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu
65 70 75 80

CO
OFFICE

GAT CTG GCC AAG AGG AGC AAG CTT GAA GCT CAG CCT TTT GCT CAT CTC
288

Asp Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu
85 90 95

ACT ATT AAT GCC ACC GAC ATC CCA TCT GGT TCC CAT AAA GTG AGT CTG
336

Thr Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu
100 105 110

TCC TCT TGG TAC CAT GAT CGG GGG TGG GGT AAG ATC TCC AAC ATG ACT
384

Ser Ser Trp Tyr His Asp Arg Gly Trp Gly Lys Ile Ser Asn Met Thr
115 120 125

TTT AGC AAT GGA AAA CTA ATA GTT AAT CAG GAT GGC TTT TAT TAC CTG
432

Phe Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu
130 135 140

TAT GCC AAC ATT TGC TTT CGA CAT CAT GAA ACT TCA GGA GAC CTA GCT
480

Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu Ala
145 150 155 160

ACA GAG TAT CTT CAA CTA ATG GTG TAC GTC ACT AAA ACC AGC ATC AAA
528

Thr Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys
165 170 175

ATC CCA AGT TCT CAT ACC CTG ATG AAA GGA GGA AGC ACC AAG TAT TGG
576

Ile Pro Ser Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp
180 185 190

TCA GGG AAT TCT GAA TTC CAT TTT TAT TCC ATA AAC GTT GGT GGA TTT
624

Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe
195 200 205

TTT AAG TTA CGG TCT GGA GAG GAA ATC AGC ATC GAG GTC TCC AAC CCC
672

Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro
210 215 220

TCC TTA CTG GAT CCG GAT CAG GAT GCA ACA TAC TTT GGG GCT TTT AAA

720

Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys

225 230 235 240

GTT CGA GAT ATA GAT TGA GCCCCAGTTT TTGGAGTGTT ATGTATTTC

768

Val Arg Asp Ile Asp *

245

TGGATGTTTG GAAACATTTT TTAACAACAG CCAAGAAAGA TGTATATAGG

TGTGTGAGAC 828

TACTAAGAGG CATGGCCCCA CGGTACACGA CTCAGTATCC ATGCTCTTGA

CCTTGTAGAG 888

AACACGCGTA TTTACAGCCA GTGGGAGATG TTAGACTCAT GGTGTGTTAC

ACAATGGTTT 948

TTAAATTTTG TAATGAATTC CTAGAATTAA ACCAGATTGG AGCAATTACG

GGTTGACCTT 1008

ATGAGAAACT GCATGTGGGC TATGGGAGGG GTTGGTCCCT GGTCATGTGC

CCCTTCGCAG 1068

CTGAAGTGA GAGGGTGTCA TCTAGCGCAA TTGAAGGATC ATCTGAAGGG

GCAAATTCTT 1128

TTGAATTGTT ACATCATGCT GGAACCTGCA AAAAATACTT TTTCTAATGA

GGAGAGAAAA 1188

TATATGTATT TTTATATAAT ATCTAAAGTT ATATTTCAGA TGTAATGTTT

TCTTTGCAAA 1248

GTATTGTAAA TTATATTTGT GCTATAGTAT TTGATTCAAA ATATTAAAA

ATGTCTTGCT 1308

GTTGACATAT TTAATGTTTT AAATGTACAG ACATATTTAA CTGGTGCACT

TTGTAAATTC 1368

CCTGGGGAAA ACTTGCAGCT AAGGAGGGGA AAAAATGTTG TTTCCTAATA

TCAAATGCAG 1428

TATATTTCTT CGTTCTTTTT AAGTTAATAG ATTTTTCAG ACTTGTCAG

CCTGTGCAAA 1488

AAAATTAAAA TGGATGCCTT GAATAATAAG CAGGATGTTG GCCACCAGGT

GCCTTTCAAA 1548

TTAGAAACT AATTGACTTT AGAAAGCTGA CATTGCCAAA AAGGATACAT
AATGGGCCAC 1608

TGAAATCTGT CAAGAGTAGT TATATAATTG TTGAACAGGT GTTTTCCAC
AAGTGCCGCA 1668

AATTGTACCT TTTTTGTTT TTTTCAAAT AGAAAAGTTA TTAGTGGTTT
ATCAGCAAAA 1728

AAGTCCAATT TTAATTTAGT AAATGTTATC TTATACTGTA CAATAAAAAC
ATTGCCTTTG 1788

AATGTTAATT TTTTGGTACA AAAGTCGACG GCCGC 1823

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Gly Thr His Cys Ile Tyr
1 5 10 15

Arg Ile Leu Arg Leu His Glu Asn Ala Asp Phe Gln Asp Thr Thr Leu
20 25 30

Glu Ser Gln Asp Thr Lys Leu Ile Pro Asp Ser Cys Arg Arg Ile Lys
35 40 45

Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly
50 55 60

Ser Gln His Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu
65 70 75 80

Asp Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu
85 90 95

Thr Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu
100 105 110

Ser Ser Trp Tyr His Asp Arg Gly Trp Gly Lys Ile Ser Asn Met Thr
115 120 125

Phe Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu
130 135 140

Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu Ala
145 150 155 160

Thr Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys
165 170 175

Ile Pro Ser Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp
180 185 190

Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe
195 200 205

Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro
210 215 220

Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys
225 230 235 240

Val Arg Asp Ile Asp *
245

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mus musculus

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 142..1092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCCACGTCCC GGGGAGCCAC TGCCAGGACC TTTGTGAACC GGTCGGGGCG
GGGGCCGTGG 60

CGGAGTCTGC TCGGCGGTGG GTGGCCCGAG AAGGGAGAGA ACGATCGCGG
AGCAGGGCGC 120

CCGAAGTCCG GGC GCCGCGC C ATG CGC CGG GCC AGC CGA GAC TAC GGC AAG
171

Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys
250 255

TAC CTG CGC AGC TCG GAA GAG ATG GGC AGC GGC CCC GGC GTC CCA CAC
219

Tyr Leu Arg Ser Ser Glu Glu Met Gly Ser Gly Pro Gly Val Pro His
260 265 270

GAA GGT CCG CTG CAC CCC GCG CCT TCT GCA CCG GCT CCG GCG CCG CCA
267

Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro
275 280 285

CCC GCC GCC TCC CGC TCC ATG TTC CTG GCC CTC CTG GGG CTG GGA CTG
315

Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu Leu Gly Leu Gly Leu
290 295 300

GGC CAG GTG GTC TGC AGC ATC GCT CTG TTC CTG TAC TTT CGA GCG CAG
363

Gly Gln Val Val Cys Ser Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln
305 310 315 320

ATG GAT CCT AAC AGA ATA TCA GAA GAC AGC ACT CAC TGC TTT TAT AGA
411

Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr His Cys Phe Tyr Arg
325 330 335

ATC CTG AGA CTC CAT GAA AAC GCA GGT TTG CAG GAC TCG ACT CTG GAG
459

Ile Leu Arg Leu His Glu Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu
340 345 350

AGT GAA GAC ACA CTA CCT GAC TCC TGC AGG AGG ATG AAA CAA GCC TTT
507

Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg Met Lys Gln Ala Phe
355 360 365

CAG GGG GCC GTG CAG AAG GAA CTG CAA CAC ATT GTG GGG CCA CAG CGC
555

Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly Pro Gln Arg
370 375 380

TTC TCA GGA GCT CCA GCT ATG ATG GAA GGC TCA TGG TTG GAT GTG GCC
603

Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser Trp Leu Asp Val Ala
385 390 395 400

CAG CGA GGC AAG CCT GAG GCC CAG CCA TTT GCA CAC CTC ACC ATC AAT
651

Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn
405 410 415

GCT GCC AGC ATC CCA TCG GGT TCC CAT AAA GTC ACT CTG TCC TCT TGG
699

Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp
420 425 430

TAC CAC GAT CGA GGC TGG GCC AAG ATC TCT AAC ATG ACG TTA AGC AAC
747

Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn
435 440 445

GGA AAA CTA AGG GTT AAC CAA GAT GGC TTC TAT TAC CTG TAC GCC AAC
795

Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn
450 455 460

ATT TGC TTT CGG CAT CAT GAA ACA TCG GGA AGC GTA CCT ACA GAC TAT
843

Ile Cys Phe Arg His His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr
465 470 475 480

CTT CAG CTG ATG GTG TAT GTC GTT AAA ACC AGC ATC AAA ATC CCA AGT
891

Leu Gln Leu Met Val Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser
485 490 495

TCT CAT AAC CTG ATG AAA GGA GGG AGC ACG AAA AAC TGG TCG GGC AAT

939

Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn
500 505 510

TCT GAA TTC CAC TTT TAT TCC ATA AAT GTT GGG GGA TTT TTC AAG CTC 987
Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu
515 520 525

CGA GCT GGT GAA GAA ATT AGC ATT CAG GTG TCC AAC CCT TCC CTG CTG
1035
Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu
530 535 540

GAT CCG GAT CAA GAT GCG ACG TAC TTT GGG GCT TTC AAA GTT CAG GAC
1083
Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp
545 550 555 560

ATA GAC TGA GACTCATTTC GTGGAACATT AGCATGGATG TCCTAGATGT
1132
Ile Asp *

TTGGAAACTT CTAAAAAAT GGATGATGTC TATACATGTG TAAGACTACT
AAGAGACATG 1192

GCCCACGGTG TATGAAACTC ACAGCCCTCT CTCTTGAGCC CTGTACAGGT
TGTGTATATG 1252

TAAAGTCCAT AGGTGATGTT AGATTCATGG TGATTACACA ACGGTTTTAC
AATTTTGTAA 1312

TGATTTCTTA GAATTGAACC AGATTGGGAG AGGTATTCCG ATGCTTATGA
AAAACCTTACA 1372

CGTGAGCTAT GGAAGGGGGT CACAGTCTCT GGTCTAACCC CTGGACATGT
GCCACTGAGA 1432

ACCTTGAAAT TAAGAGGATG CCATGTCATT GCATAGAAAT GATAGTGTGA
AGGGTTAAGT 1492

TCTTTTGAAT TGTTACATTG CGCTGGGACC TGCAAATAAG TTCTTTTTTT
CTAATGAGGA 1552

GAAAAATATA TGTATTTTAA TATAATGTCT AAAGTTATAT TTCAGGTGTA
ATGTTTTCTG 1612

TGCAAAGTTT TGTA AATTAT ATTTGTGCTA TAGTATTTGA TTCAA AATAT
TTAAAAATGT 1672

CTCACTGTTG ACATATTTAA TGTTTTAAAT GTACAGATGT ATTAACTGG
TGCAC TTTGT 1732

AATTCCCCTG AAGGTACTCG TAGCTAAGGG GGCAGAATAC TGTTTCTGGT
GACCACATGT 1792

AGTTTATTTT TTTATTTCTT TTA ACTTAAT AGAGTCTTCA GACTTG TCAA
AACTATGCAA 1852

GCAAAATAAA TAAATAAAAA TAAAATGAAT ACCTTGAATA ATAAGTAGGA
TGTTGGTCAC 1912

CAGGTGCCTT TCAAATTTAG AAGCTAATTG ACTTTAGGAG CTGACATAGC
CAAAAAGGAA 1972

CATAATAGGC TACTGAAATC TGTCAGGAGT ATTTATGCAA TTATTGAACA
GGTGTCTTTT 2032

TTTACAAGAG CTACAAATTG TAAATTTTGG TTTCTTTTTT TTCCCATAGA
AAATGTACTA 2092

TAGTTTATCA GCCAAAAAAC AATCCACTTT TTAATTTAGT GAAAGTTATT
TTATTATACT 2152

GTACAATAAA AGCATTGTCT CTGAATGTTA ATTTTTTGGT ACAAAAAATA
AATTTGTACG 2212

AAAAAAAAAA AAAAAAAAAA AAAAA

2237

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu

1

5

10

15

Glu Met Gly Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His Pro
20 25 30

Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser
35 40 45

Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser
50 55 60

Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile
65 70 75 80

Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu
85 90 95

Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro
100 105 110

Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys
115 120 125

Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala
130 135 140

Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu
145 150 155 160

Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser
165 170 175

Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp
180 185 190

Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn
195 200 205

Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His
210 215 220

Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr
225 230 235 240

Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys
245 250 255

Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr

260	265	270
Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile		
275	280	285
Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala		
290	295	300
Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp *		
305	310	315

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Gln	Gln	Pro	Met	Asn	Tyr	Pro	Cys	Pro	Gln	Ile	Phe	Trp	Val	Asp
1		5		10		15									

Ser	Ser	Ala	Thr	Ser	Ser	Trp	Ala	Pro	Pro	Gly	Ser	Val	Phe	Pro	Cys
	20			25				30							

Pro	Ser	Cys	Gly	Pro	Arg	Gly	Pro	Asp	Gln	Arg	Arg	Pro	Pro	Pro	Pro
	35			40				45							

Pro	Pro	Pro	Val	Ser	Pro	Leu	Pro	Pro	Pro	Ser	Gln	Pro	Leu	Pro	Leu
	50			55				60							

Pro	Pro	Leu	Thr	Pro	Leu	Lys	Lys	Lys	Asp	His	Asn	Thr	Asn	Leu	Trp
	65			70			75		80						

Leu Pro Val Val Phe Phe Met Val Leu Val Ala Leu Val Gly Met Gly

85	90	95
Leu Gly Met Tyr Gln Leu Phe His Leu Gln Lys Glu Leu Ala Glu Leu		
100	105	110
Arg Glu Phe Thr Asn Gln Ser Leu Lys Val Ser Ser Phe Glu Lys Gln		
115	120	125
Ile Ala Asn Pro Ser Thr Pro Ser Glu Lys Lys Glu Pro Arg Ser Val		
130	135	140
Ala His Leu Thr Gly Asn Pro His Ser Arg Ser Ile Pro Leu Glu Trp		
145	150	155 160
Glu Asp Thr Tyr Gly Thr Ala Leu Ile Ser Gly Val Lys Tyr Lys Lys		
165	170	175
Gly Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe Val Tyr Ser Lys		
180	185	190
Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn Gln Pro Leu Asn His Lys		
195	200	205
Val Tyr Met Arg Asn Ser Lys Tyr Pro Glu Asp Leu Val Leu Met Glu		
210	215	220
Glu Lys Arg Leu Asn Tyr Cys Thr Thr Gly Gln Ile Trp Ala His Ser		
225	230	235 240
Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Ser Ala Asp His Leu Tyr		
245	250	255
Val Asn Ile Ser Gln Leu Ser Leu Ile Asn Phe Glu Glu Ser Lys Thr		
260	265	270
Phe Phe Gly Leu Tyr Lys Leu		
275		

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Pro Ser Ser Gly Ala Leu Lys Asp Leu Ser Phe Ser Gln His Phe
1 5 10 15

Arg Met Met Val Ile Cys Ile Val Leu Leu Gln Val Leu Leu Gln Ala
20 25 30

Val Ser Val Ala Val Thr Tyr Met Tyr Phe Thr Asn Glu Met Lys Gln
35 40 45

Leu Gln Asp Asn Tyr Ser Lys Ile Gly Leu Ala Cys Phe Ser Lys Thr
50 55 60

Asp Glu Asp Phe Trp Asp Ser Thr Asp Gly Glu Ile Leu Asn Arg Pro
65 70 75 80

Cys Leu Gln Val Lys Arg Gln Leu Tyr Gln Leu Ile Glu Glu Val Thr
85 90 95

Leu Arg Thr Phe Gln Asp Thr Ile Ser Thr Val Pro Glu Lys Gln Leu
100 105 110

Ser Thr Pro Pro Leu Pro Arg Gly Gly Arg Pro Gln Lys Val Ala Ala
115 120 125

His Ile Thr Gly Ile Thr Arg Arg Ser Asn Ser Ala Leu Ile Pro Ile
130 135 140

Ser Lys Asp Gly Lys Thr Leu Gly Gln Lys Ile Glu Ser Trp Glu Ser
145 150 155 160

Ser Arg Lys Gly His Ser Phe Leu Asn His Val Leu Phe Arg Asn Gly
165 170 175

Glu Leu Val Ile Glu Gln Glu Gly Leu Tyr Tyr Ile Tyr Ser Gln Thr
180 185 190

Tyr Phe Arg Phe Gln Glu Ala Glu Asp Ala Ser Lys Met Val Ser Lys
195 200 205

Asp Lys Val Arg Thr Lys Gln Leu Val Gln Tyr Ile Tyr Lys Tyr Thr
210 215 220

Ser Tyr Pro Asp Pro Ile Val Leu Met Lys Ser Ala Arg Asn Ser Cys
225 230 235 240

Trp Ser Arg Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly
245 250 255

Leu Phe Glu Leu Lys Lys Asn Asp Arg Ile Phe Val Ser Val Thr Asn
260 265 270

Glu His Leu Met Asp Leu Asp Gln Glu Ala Ser Phe Phe Gly Ala Phe
275 280 285

Leu Ile Asn
290

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Gly Thr Arg Gly Leu Gln Gly Leu Gly Gly Arg Pro Gln Gly Arg
1 5 10 15

Gly Cys Leu Leu Leu Ala Val Ala Gly Ala Thr Ser Leu Val Thr Leu
20 25 30

Leu Leu Ala Val Pro Ile Thr Val Leu Ala Val Leu Ala Leu Val Pro
35 40 45

Gln Asp Gln Gly Arg Arg Val Glu Lys Ile Ile Gly Ser Gly Ala Gln
50 55 60

Ala Gln Lys Arg Leu Asp Asp Ser Lys Pro Ser Cys Ile Leu Pro Ser
65 70 75 80

Pro Ser Ser Leu Ser Glu Thr Pro Asp Pro Arg Leu His Pro Gln Arg
85 90 95

Ser Asn Ala Ser Arg Asn Leu Ala Ser Thr Ser Gln Gly Pro Val Ala
100 105 110

Gln Ser Ser Arg Glu Ala Ser Ala Trp Met Thr Ile Leu Ser Pro Ala
115 120 125

Ala Asp Ser Thr Pro Asp Pro Gly Val Gln Gln Leu Pro Lys Gly Glu
130 135 140

Pro Glu Thr Asp Leu Asn Pro Glu Leu Pro Ala Ala His Leu Ile Gly
145 150 155 160

Ala Trp Met Ser Gly Gln Gly Leu Ser Trp Glu Ala Ser Gln Glu Glu
165 170 175

Ala Phe Leu Arg Ser Gly Ala Gln Phe Ser Pro Thr His Gly Leu Ala
180 185 190

Leu Pro Gln Asp Gly Val Tyr Tyr Leu Tyr Cys His Val Gly Tyr Arg
195 200 205

Gly Arg Thr Pro Pro Ala Gly Arg Ser Arg Ala Arg Ser Leu Thr Leu
210 215 220

Arg Ser Ala Leu Tyr Arg Ala Gly Gly Ala Tyr Gly Arg Gly Ser Pro
225 230 235 240

Glu Leu Leu Leu Glu Gly Ala Glu Thr Val Thr Pro Val Val Asp Pro
245 250 255

Ile Gly Tyr Gly Ser Leu Trp Tyr Thr Ser Val Gly Phe Gly Gly Leu
260 265 270

Ala Gln Leu Arg Ser Gly Glu Arg Val Tyr Val Asn Ile Ser His Pro

275	280	285	
Asp Met Val Asp Tyr Arg Arg Gly Lys Thr Phe Phe Gly Ala Val Met			
290	295	300	
Val Gly			
305			

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ser Thr Glu Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Ala			
1	5	10	15
Leu Pro Gln Lys Met Gly Gly Phe Gln Asn Ser Arg Arg Cys Leu Cys			
20	25	30	
Leu Ser Leu Phe Ser Phe Leu Leu Val Ala Gly Ala Thr Thr Leu Phe			
35	40	45	
Cys Leu Leu Asn Phe Gly Val Ile Gly Pro Gln Arg Asp Glu Lys Phe			
50	55	60	
Pro Asn Gly Leu Pro Leu Ile Ser Ser Met Ala Gln Thr Leu Thr Leu			
65	70	75	80
Arg Ser Ser Ser Gln Asn Ser Ser Asp Lys Pro Val Ala His Val Val			
85	90	95	
Ala Asn His Gln Val Glu Glu Gln Leu Glu Trp Leu Ser Gln Arg Ala			

100	105	110
Asn Ala Leu Leu Ala Asn Gly Met Asp Leu Lys Asp Asn Gln Leu Val		
115	120	125
Val Pro Ala Asp Gly Leu Tyr Leu Val Tyr Ser Gln Val Leu Phe Lys		
130	135	140
Gly Gln Gly Cys Pro Asp Tyr Val Leu Leu Thr His Thr Val Ser Arg		
145	150	155
		160
Phe Ala Ile Ser Tyr Gln Glu Lys Val Asn Leu Leu Ser Ala Val Lys		
165	170	175
Ser Pro Cys Pro Lys Asp Thr Pro Glu Gly Ala Glu Leu Lys Pro Trp		
180	185	190
Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp		
195	200	205
Gln Leu Ser Ala Glu Val Asn Leu Pro Lys Tyr Leu Asp Phe Ala Glu		
210	215	220
Ser Gly Gln Val Tyr Phe Gly Val Ile Ala Leu		
225	230	235

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PRIMER"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGAAGATCC TGACCGAGCG

20

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PRIMER"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TACTTGCGCT GAGGAGGAGC

20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PRIMER"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCTGAGACTC CATGAAAACG C

21

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PRIMER"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TAACCCTTAG TTTCCGTTG C

21

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PRIMER"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACCCAGATGG ACTTCTGTGG

20

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PRIMER"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTTCCTTCGA CGTGCTAACG

20

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GTAATGATCA GTCAACGGGG GAC

23

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCAGCAAGCT TGCAACCTTA ACCA

24

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTGGCAACTG GACTTCCAGC G

21

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GCGTTGACTC GAAGGCTCCC G

21